

```

5'  AAA CCT TCA CCT CTC      18  ATG CTG AAG CTC ACA CCC TTG CCC TCC AAG ATG AAG GTT
      M  L  K  L  T  P  L  P  S  K  M  K  V

      63  GCG CTT CTG      72  TGC CTG CTG CTC ATG GCA GCC ACT TTC AGC CCT CAG GGA
      S  A  A  L  L  C  L  L  L  M  A  A  T  F  S  P  Q  G

      117  GCT CAG CCA GAT TCA GTT TCC ATT CCA ATC ACC TGC TGC TTT AAC GTG ATC
      L  A  Q  P  D  S  V  S  I  P  I  T  C  C  F  N  V  I

      171  AGG AAA ATT CCT ATC CAG AGG CTG GAG AGC TAC ACA AGA ATC ACC AAC ATC
      N  R  K  I  P  I  Q  R  L  E  S  Y  T  R  I  T  N  I

      225  TGT CCC AAG GAA GCT GTG ATC TTC AAG ACC AAA CGG GGC AAG GAG GTC TGT
      Q  C  P  K  E  A  V  I  F  K  T  K  R  G  K  E  V  C

      279  GAC CCC AAG GAG AGA TGG GTC AGG GAT TCC ATG AAG CAT CTG GAC CAA ATA
      A  D  P  K  E  R  W  V  R  D  S  M  K  H  L  D  Q  I

      333  CAA AAT CTG AAG CCA TGA GCC TTC ATA CAT GGA CTG AGA GTC AGA GCT TGA
      F  Q  N  L  K  P

      387  AAA GCT TAT TTA TTT TCC CCA ACC TCC CCC AGG TGC AGT GTG ACA TTA TTT
      AGA

      441  AAC ATC CAC AAA GAG ATT ATT TTT AAA TAA TTT AAA GCA TAA TAT TTC
      TAT

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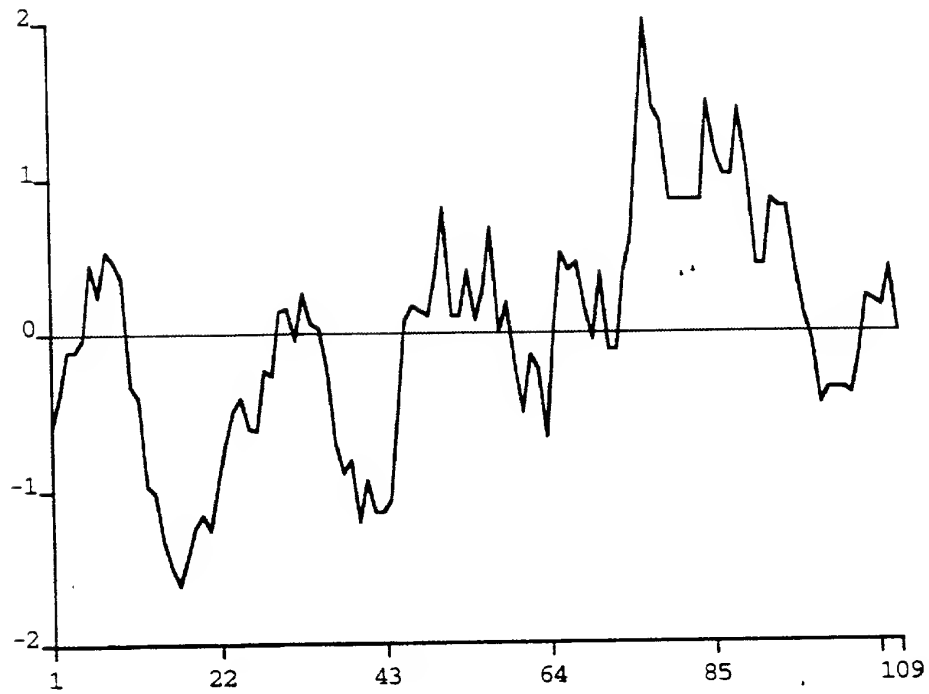
FIGURE 1A

TTA	AAA	495	AGT	ATT	TAA	504	TTA	TAT	TTA	513	AGT	TGT	TGA	522	TGT	TTT	AAC	531	TCT	ATC	TGT	540	CAT
ACA	TCC	549	TAG	TGA	ATG	558	TAA	AAT	GCA	567	AAA	TCC	TGG	576	TGA	TGT	GTT	585	TTT	TGT	TTT	594	TGT
TTT	CCT	603	GTG	AGC	TCA	612	ACT	AAG	TTC	621	ACG	GCC	AAA	630	NGT	CAT	TGT	639	TCT	CCC	TCC	648	TAC
CNG	TNC	657	GTA	GTG	TTG	666	TGG	GGT	CCT	675	CCC	NTG	GAT	684	CAT	CAA	GGT	693	GAA	ACA	CTT	702	AGG
TAT	TCT	711	TTG	GCA	ATC	720	AGT	GCT	CCT	729	GTA	AGT	CAA	738	ATG	TGT	GCT	747	TTG	TAC	TGC	756	TGT
TGT	TGA	765	AAT	TGA	NGT	774	TAC	TGT	ANA	783	TAA	CTA	TGG	792	AAT	TTT	GAA	801	AAA	AAA	TTT	810	CAA
AAA	GAA	819	AAA	NAT	ATA	828	TAT	AAT	TTA	837	AAA	CTA	AAA	846	AAA	AAA	AAA	855	AAA	A	3'		

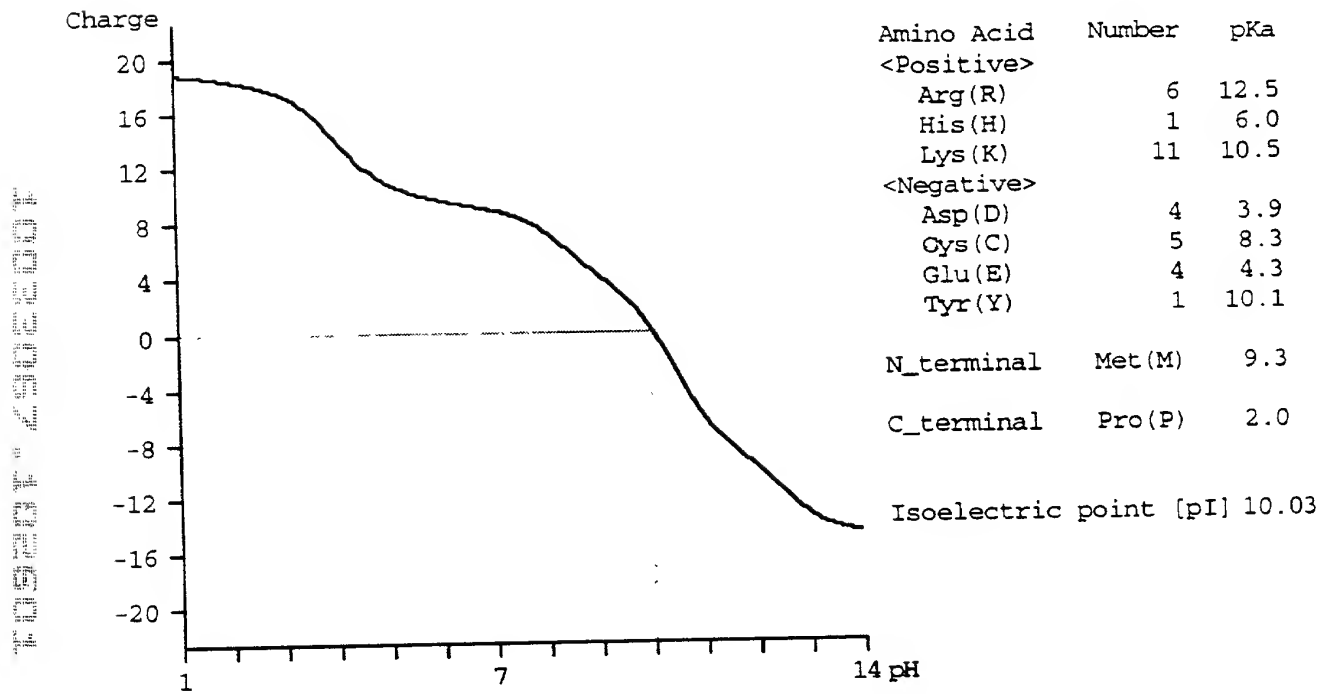
FIGURE 1B

1	M	L	K	L	T	P	L	P	S	K	M	K	V	S	A	A	L	L	C	L	L	L	M	A	A	T	F	S	P	Q	965517
1	M	W	K	P	M	P	S	P	S	N	M	K	A	S	A	A	L	L	C	L	L	L	T	A	A	A	F	S	P	Q	GI 288397
1	M	-	-	-	-	-	-	-	-	-	-	K	V	S	A	A	L	L	C	L	L	L	I	A	A	T	F	I	P	Q	GI 338809
31	G	L	A	Q	P	D	S	V	S	I	P	I	T	C	C	F	N	V	I	N	R	K	I	P	I	Q	R	L	E	S	965517
31	G	L	A	Q	P	V	G	I	N	T	S	T	T	C	C	Y	R	F	I	N	K	K	I	P	K	Q	R	L	E	S	GI 288397
21	G	L	A	Q	P	D	A	I	N	A	P	V	T	C	C	Y	N	F	T	N	R	K	I	S	V	Q	R	L	A	S	GI 338809
61	Y	T	R	I	T	N	I	Q	C	P	K	E	A	V	I	F	K	T	K	R	G	K	E	V	C	A	D	P	K	E	965517
61	Y	R	R	T	T	S	S	H	C	P	R	E	A	V	I	F	K	T	K	L	D	K	E	I	C	A	D	P	T	Q	GI 288397
51	Y	R	R	I	T	S	S	K	C	P	K	E	A	V	I	F	K	T	I	V	A	K	E	I	C	A	D	P	K	Q	GI 338809
91	R	W	V	R	D	S	M	K	H	L	D	Q	I	F	Q	N	L	K	P	965517											
91	K	W	V	Q	D	F	M	K	H	L	D	K	K	T	Q	T	P	K	L	GI 288397											
81	K	W	V	Q	D	S	M	D	H	L	D	K	Q	T	Q	T	P	K	T	GI 338809											

FIGURE 2



**FIGURE 3**



**FIGURE 4**

The Electronic Northern for Clone: 965517  
and Stringency = 50

Library	Lib Description	Abun	Pct Abun
<u>PANCDIT03</u>	pancreas, NIDDM, 57 M	1	0.145
<u>MMLR1DT01</u>	macrophages (adher PBMNC), M/F, 24-hr MLR	4	0.094
<u>MMLR3DT01</u>	macrophages (adher PBMNC), M/F, 72-hr MLR	2	0.066
<u>MPHGLPT02</u>	macrophages (adher PBMNC), M/F, treated LPS	1	0.045
<u>TMLR3DT01</u>	lymphocytes (non-adher PBMNC), M, 96-hr MLR	2	0.045
<u>BLADTUT02</u>	bladder tumor, carcinoma, 80 F	1	0.030
<u>SYNORAT05</u>	synovium, knee, rheumatoid, 62 F	1	0.028
<u>LUNGNOM01</u>	lung, 72 M, WM	1	0.026
<u>MPHGNOT03</u>	macrophages (adher PBMNC), M/F	2	0.025
<u>BRSTNOT05</u>	breast, 58 F, match to BRSTTUT03	1	0.015

FIGURE 5